

RAW SEQUENCE LISTING

EFS

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Application Serial Number: 10/511,813
Source: FW16
Date Processed by STIC: 3/15/07

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IFW16

RAW SEQUENCE LISTING

DATE: 03/15/2007

PATENT APPLICATION: US/10/511,813

TIME: 14:38:29

Input Set : N:\efs\03_15_07\10511813_efs\SEQUENCE_LISTING.txt

Output Set: N:\CRF4\03152007\J511813.raw

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3 <110> APPLICANT: COY, Johannes
5 <120> TITLE OF INVENTION: Compositions and methods for detection and treatment of
6   proliferative abnormalities associated with overexpression of
7   human transketolase like-1 gene
9 <130> FILE REFERENCE: 4007-008
11 <140> CURRENT APPLICATION NUMBER: 10/511,813
12 <141> CURRENT FILING DATE: 2004-10-19
14 <150> PRIOR APPLICATION NUMBER: PCT/EP03/03827
15 <151> PRIOR FILING DATE: 2003-04-12
17 <150> PRIOR APPLICATION NUMBER: EP 02008831.6
18 <151> PRIOR FILING DATE: 2002-04-19
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn version 3.4
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2531
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
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34 gcaccttgca ggtgttgcaa gatatggcca gccgcttgcg aatccattcc atcagggccca      180
36 catgctccac gagctccggc caccctacat catgtagcag ttcttctgag atcatgtctg      240
38 tgctgttctt ctacatcatg aggtacaagc agtcagatcc agagaatccg gacaacgacc      300
40 gatttgtcct cgcaaagaga ctgtcgtttg tggatgtggc aacaggatgg ctcggaacaag      360
42 gactgggagt tgcattgtga atggcatata ctggcaagta cttcgacagg gccagctacc      420
44 ggggtgtctg cctcatgagt gatggcgagt cctcagaagg ctctgtctgg gaggcaatgg      480
46 cctttgcttc ctactacagt ctggacaatc ttgtggcaat ctttgatgtg aaccgcctgg      540
48 gacacagtgg tgcattgccc gccgagcact gcataaacat ctatcagagg cgctgcgaag      600
50 cctttgggtg gaacacttat gtggtggacg gccggggacgt ggaggcactg tgccaggtat      660
52 tctggcaggc ttctcagggtg aagcacaagc ccactgctgt ggtggccaag accttcaagg      720
54 gccggggcac cccaagtatt gaggatgcag aaagttggca tgcaaagcca atgccgagag      780
56 aaagagcaga tgccattatc aaattaattg agagccagat acagaccagc aggaatcttg      840
58 acccacagcc ccccatagag gactcacctg aagtcaacat cacagatgta aggatgacct      900
60 ctccacctga ttacagagtt ggtgacaaga tagctactcg gaaagcatgc ggtctggctc      960
62 tggctaagct gggctacgag aacaacagag tegtgtgtgt ggatgggtgac accaggtact     1020
64 ctactttctc tgagatattc aacaaggagt accctgagcg cttcatcgag tgctttatgg      1080
66 ctgaacaaaa catggtgagc gtggctctgg gctgtgcctc cctgtggacgg accattgctt      1140
68 ttgctagcac ctttgcgtgc tttctgactc gagcatttga tcacatccgg ataggaggcc      1200
70 tcgctgagag caacatcaac attattgggt cccactgtgg ggtatctgtt ggtgacgatg      1260
72 gtgcttccca gatggccctg gaggatatag ccatgttccg aaccattccc aagtgcacga      1320
74 tcttctaccc aactgatgcc gtctccacgg agcatgctgt tgctctggca gccaatgcca      1380
76 aggggatgtg cttcattcgg accaccggac cagaaactat ggttatttac accccacaag      1440
78 aacgctttga gatcggacag gccaaaggtcc tccgccactg tgtcagtgac aaggtcacag      1500

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82 aagatatttt tatccgtgtc atcgacctgt ttaccattaa acctctggat gtcgccacca 1620
84 tcgtctccag tgcaaaagcc acagagggcc ggatcattac agtggaggat cactaccgcg 1680
86 aaggtggcat cggggaagct gtctgcgcag ccgtctccat ggatcctgac attcaggttc 1740
88 attcgctggc agtgtcggga gtgccccaga gtgggaagtc cgaggaattg ctggatatgt 1800
90 atggaattag tgccagacat atcatagtgg ccgtgaaatg catgttgctg aactaaaata 1860
92 gctgtagacc ttggtctttt ggccctctta ccctgtgttt atgtttgttc caaaaccatc 1920
94 atttaaactc ctactgtcac attttgtttc ttaaaagcaa agccagctaa caccttcatt 1980
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100 aggtaacaaa acaaccacct gatagtaagt tttctgataa gactatagat aagtggtaga 2160
102 ggtaatcaat tcttccgaag tgtttccttc gtgaataact ggtagaggta atagtttttt 2220
104 caatgtatct cttcatgag taaagaaaat gtggattgaa gtatagattc cagtagccta 2280
106 gtttccacag cacgataaca ccatgacgcc tactgtgtgt cccaccttgg gattctgtgt 2340
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110 cacgtttgag aggtgtgcag gcagcagcga aagcttgtaa ggatgtcctg tgctgcttgt 2460
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118 <211> LENGTH: 596
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
122 <400> SEQUENCE: 2
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125 1 5 10 15
128 Asp Arg Gly Thr Leu Gln Val Leu Gln Asp Met Ala Ser Arg Leu Arg
129 20 25 30
132 Ile His Ser Ile Arg Ala Thr Cys Ser Thr Ser Ser Gly His Pro Thr
133 35 40 45
136 Ser Cys Ser Ser Ser Ser Glu Ile Met Ser Val Leu Phe Phe Tyr Ile
137 50 55 60
140 Met Arg Tyr Lys Gln Ser Asp Pro Glu Asn Pro Asp Asn Asp Arg Phe
141 65 70 75 80
144 Val Leu Ala Lys Arg Leu Ser Phe Val Asp Val Ala Thr Gly Trp Leu
145 85 90 95
148 Gly Gln Gly Leu Gly Val Ala Cys Gly Met Ala Tyr Thr Gly Lys Tyr
149 100 105 110
152 Phe Asp Arg Ala Ser Tyr Arg Val Phe Cys Leu Met Ser Asp Gly Glu
153 115 120 125
156 Ser Ser Glu Gly Ser Val Trp Glu Ala Met Ala Phe Ala Ser Tyr Tyr
157 130 135 140
160 Ser Leu Asp Asn Leu Val Ala Ile Phe Asp Val Asn Arg Leu Gly His
161 145 150 155 160
164 Ser Gly Ala Leu Pro Ala Glu His Cys Ile Asn Ile Tyr Gln Arg Arg
165 165 170 175
168 Cys Glu Ala Phe Gly Trp Asn Thr Tyr Val Val Asp Gly Arg Asp Val
169 180 185 190
172 Glu Ala Leu Cys Gln Val Phe Trp Gln Ala Ser Gln Val Lys His Lys
173 195 200 205

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176 Pro Thr Ala Val Val Ala Lys Thr Phe Lys Gly Arg Gly Thr Pro Ser
177      210      215      220
180 Ile Glu Asp Ala Glu Ser Trp His Ala Lys Pro Met Pro Arg Glu Arg
181 225      230      235      240
184 Ala Asp Ala Ile Ile Lys Leu Ile Glu Ser Gln Ile Gln Thr Ser Arg
185      245      250      255
188 Asn Leu Asp Pro Gln Pro Pro Ile Glu Asp Ser Pro Glu Val Asn Ile
189      260      265      270
192 Thr Asp Val Arg Met Thr Ser Pro Pro Asp Tyr Arg Val Gly Asp Lys
193      275      280      285
196 Ile Ala Thr Arg Lys Ala Cys Gly Leu Ala Leu Ala Lys Leu Gly Tyr
197      290      295      300
200 Ala Asn Asn Arg Val Val Val Leu Asp Gly Asp Thr Arg Tyr Ser Thr
201 305      310      315      320
204 Phe Ser Glu Ile Phe Asn Lys Glu Tyr Pro Glu Arg Phe Ile Glu Cys
205      325      330      335
208 Phe Met Ala Glu Gln Asn Met Val Ser Val Ala Leu Gly Cys Ala Ser
209      340      345      350
212 Arg Gly Arg Thr Ile Ala Phe Ala Ser Thr Phe Ala Ala Phe Leu Thr
213      355      360      365
216 Arg Ala Phe Asp His Ile Arg Ile Gly Gly Leu Ala Glu Ser Asn Ile
217      370      375      380
220 Asn Ile Ile Gly Ser His Cys Gly Val Ser Val Gly Asp Asp Gly Ala
221 385      390      395      400
224 Ser Gln Met Ala Leu Glu Asp Ile Ala Met Phe Arg Thr Ile Pro Lys
225      405      410      415
228 Cys Thr Ile Phe Tyr Pro Thr Asp Ala Val Ser Thr Glu His Ala Val
229      420      425      430
232 Ala Leu Ala Ala Asn Ala Lys Gly Met Cys Phe Ile Arg Thr Thr Arg
233      435      440      445
236 Pro Glu Thr Met Val Ile Tyr Thr Pro Gln Glu Arg Phe Glu Ile Gly
237      450      455      460
240 Gln Ala Lys Val Leu Arg His Cys Val Ser Asp Lys Val Thr Val Ile
241 465      470      475      480
244 Gly Ala Gly Ile Thr Val Tyr Glu Ala Leu Ala Ala Ala Asp Glu Leu
245      485      490      495
248 Ser Lys Gln Asp Ile Phe Ile Arg Val Ile Asp Leu Phe Thr Ile Lys
249      500      505      510
252 Pro Leu Asp Val Ala Thr Ile Val Ser Ser Ala Lys Ala Thr Glu Gly
253      515      520      525
256 Arg Ile Ile Thr Val Glu Asp His Tyr Pro Gln Gly Gly Ile Gly Glu
257      530      535      540
260 Ala Val Cys Ala Ala Val Ser Met Asp Pro Asp Ile Gln Val His Ser
261 545      550      555      560
264 Leu Ala Val Ser Gly Val Pro Gln Ser Gly Lys Ser Glu Glu Leu Leu
265      565      570      575
268 Asp Met Tyr Gly Ile Ser Ala Arg His Ile Ile Val Ala Val Lys Cys
269      580      585      590
272 Met Leu Leu Asn

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276 <210> SEQ ID NO: 3
277 <211> LENGTH: 213
278 <212> TYPE: PRT
279 <213> ORGANISM: Homo sapiens
281 <400> SEQUENCE: 3
283 Ser Gly Ala Leu Pro Ala Glu His Cys Ile Asn Ile Tyr Gln Arg Arg
284 1          5          10          15
287 Cys Glu Ala Phe Gly Trp Asn Thr Tyr Val Val Asp Gly Arg Asp Val
288          20          25          30
291 Glu Ala Leu Cys Gln Val Phe Trp Gln Ala Ser Gln Val Lys His Lys
292          35          40          45
295 Pro Thr Ala Val Val Ala Lys Thr Phe Lys Gly Arg Gly Thr Pro Ser
296          50          55          60
299 Ile Glu Asp Ala Glu Ser Trp His Ala Lys Pro Met Pro Arg Glu Arg
300 65          70          75          80
303 Ala Asp Ala Ile Ile Lys Leu Ile Glu Ser Gln Ile Gln Thr Ser Arg
304          85          90          95
307 Asn Leu Asp Pro Gln Pro Pro Ile Glu Asp Ser Pro Glu Val Asn Ile
308          100         105         110
311 Thr Asp Val Arg Met Thr Ser Pro Pro Asp Tyr Arg Val Gly Asp Lys
312          115         120         125
315 Ile Ala Thr Arg Lys Ala Cys Gly Leu Ala Leu Ala Lys Leu Gly Tyr
316          130         135         140
319 Ala Asn Asn Arg Val Val Leu Asp Gly Asp Thr Arg Tyr Ser Thr
320 145         150         155         160
323 Phe Ser Glu Ile Phe Asn Lys Glu Tyr Pro Glu Arg Phe Ile Glu Cys
324          165         170         175
327 Phe Met Ala Glu Gln Asn Met Val Ser Val Ala Leu Gly Cys Ala Ser
328          180         185         190
331 Arg Gly Arg Thr Ile Ala Phe Ala Ser Thr Phe Ala Ala Phe Leu Thr
332          195         200         205
335 Arg Ala Phe Asp His
336          210
339 <210> SEQ ID NO: 4
340 <211> LENGTH: 17
341 <212> TYPE: PRT
342 <213> ORGANISM: Homo sapiens
344 <400> SEQUENCE: 4
346 Ser Arg Asn Leu Asp Pro Gln Pro Pro Ile Glu Asp Ser Pro Glu Val
347 1          5          10          15
350 Asn
354 <210> SEQ ID NO: 5
355 <211> LENGTH: 15
356 <212> TYPE: PRT
357 <213> ORGANISM: Homo sapiens
359 <400> SEQUENCE: 5
361 Tyr Ala Asn Asn Arg Val Val Val Leu Asp Gly Asp Thr Arg Tyr
362 1          5          10          15

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365 <210> SEQ ID NO: 6
366 <211> LENGTH: 20
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
370 <400> SEQUENCE: 6
371 caccttggga ttctgtgtgc 20
374 <210> SEQ ID NO: 7
375 <211> LENGTH: 20
376 <212> TYPE: DNA
377 <213> ORGANISM: Homo sapiens
379 <400> SEQUENCE: 7
380 tctcatcaca agcagcacag 20
383 <210> SEQ ID NO: 8
384 <211> LENGTH: 20
385 <212> TYPE: DNA
386 <213> ORGANISM: Homo sapiens
388 <400> SEQUENCE: 8
389 tgtgtccagt gcagtagtgg 20
392 <210> SEQ ID NO: 9
393 <211> LENGTH: 20
394 <212> TYPE: DNA
395 <213> ORGANISM: Homo sapiens
397 <400> SEQUENCE: 9
398 acacttcata cccgccctag 20
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VERIFICATION SUMMARY

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